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Strong genetic component of fibromyalgia suggested

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(HealthDay)—A genome-wide linkage scan has identified the chromosome 17p11.2-q11.2 region as the susceptibility locus for fibromyalgia, according to research published in the April issue of *Arthritis & Rheumatism*.

Lesley M. Arnold, M.D., of the University of Cincinnati College of Medicine, and colleagues genotyped members from 116 families from the Fibromyalgia Family Study and performed a genome-wide linkage scan to identify susceptibility loci for fibromyalgia.

According to the researchers, based on a 2 percent population prevalence

of fibromyalgia, the sibling recurrence risk ratio for fibromyalgia was estimated to be 13.3. Model-free linkage analysis identified one major locus for fibromyalgia at the D17S2196 and D17S1294 markers on the chromosome 17p11.2-q11.2.

"In conclusion, we detected genome-wide suggestive linkage to the chromosome 17p11.2-q11.2 region in a cohort of multi-case families from the Fibromyalgia Family Study," the authors write. "Further comprehensive sequencing analyses of the 17p11.2-q11.2 chromosome region in multi-case families are warranted to identify potential causal genetic risk variants for fibromyalgia."

One author disclosed providing expert testimony for administrative law judges of the Office of Disability Adjudication and Review of the Social Security Administration.

More information: Abstract
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